Please delete the first row of Table I. Please enter the Sequence Listing into the specification. (The Sequence Listing reflects the above-referenced amendment and does not include the first row of Table I.) The content of the paper copy and the computer readable copy is the same and includes no new matter.

With respect to Table II, HCV oligo, please insert therein --SEQ ID NO. 1--.

With respect to Table II, HCVR2 oligo, please insert therein --SEQ ID NO. 2--.

With respect to Table III, Probe C1, please insert therein --SEQ ID NO. 3--.

With respect to Table III, Probe C2, please insert therein --SEQ ID NO. 4--.

With respect to Table I, please insert therein --SEQ ID NO. 5--.

IN THE CLAIMS

Please add the following new claims, which are supported by the specification:

~~14. (or~~ 13.) The method of claim 1 wherein the ratio of the second probe to the first probe is about 2:1.

~~15. (or~~ 14.) The method of claim 1 wherein the first probe has the sequence of SEQ ID NO. 3.

~~16. (or~~ 15.) The method of claim 1 wherein the second probe has the sequence of SEQ ID NO. 4.

~~17. (OR~~ 16.) The method of claim 1 wherein the amplification method is the polymerase chain reaction and wherein a primer for use in the polymerase chain reaction has the sequence of SEQ ID NO. 1.

~~18. (OR~~ 17.) The method of claim 1 wherein the amplification method is the polymerase chain reaction and wherein a primer for use in the polymerase chain reaction has the sequence of SEQ ID NO. 2.

~~19. (or~~ 18.) The method of claim 1 wherein the target polynucleotide is a polynucleotide comprising the HCV genome.

~~20. (or~~ 19.) The method of claim 1 wherein the method of amplification is selected from the group consisting of ligase chain reaction, gap ligase chain reaction, transcription mediated amplification, nucleic acid sequence based amplification and strand displacement amplification.

(Amended) 1. A method for monitoring nucleic acid amplification comprising:

performing nucleic acid amplification on a target polynucleotide wherein the amplification is carried out using any method the method not requiring the use of an enzyme having a 5' to 3' exonuclease activity, and further comprising using a first oligonucleotide probe and a second [shorter] oligonucleotide probe, said second probe being shorter in length than said first probe, [varying in length] by about at least [about] two [2] base pairs, thereby favoring the annealing of one or both of the first or second probes to the target nucleic acid sequence over the annealing of the first and second probe to each other;

the first probe having a fluorophore;

the second probe being complementary with the first probe and having a quencher molecule capable of quenching the fluorescence of said fluorophore, the fluorophore and quencher being attached on their respective probes at positions which result[s] in the quencher molecule quenching the fluorescence of the fluorophore when the probes are hybridized to each other,

wherein the [longer] first probe binds preferentially to the target polynucleotide and when preferentially bound to the target polynucleotide the fluorescence intensity of the fluorophore is greater than the fluorescence intensity of the fluorophore when hybridized to the second probe, and